



SEQUENCE LISTING

<110> KOIBUCHI, KYOKO
NINOMIYA, DAIKI
KOJIMA, MARI
UEDA, YOICHI
MARUYAMA, JUN-ICHI
KITAMOTO, KATSUHIKO

<120> NEW AMINOPEPTIDASE AND THE GENES THEREOF

<130> 241461US0CONT

<140> 10/664,958

<141> 2003-09-22

<150> PCT/JP02/02476

<151> 2002-03-15

<150> JP 2001-078930

<151> 2001-03-19

<150> JP 2001-293348

<151> 2001-09-26

<160> 15

<170> PatentIn version 3.3

<210> 1

<211> 3383

<212> DNA

<213> Aspergillus nidulans

<400> 1
gggagaagtg tcgcaggatc gagtgtttgt cagtgtgctg gtcacggagc cgagccaggt 60
gcatattcag attgggcctg cagcatctag agtcttgatt gcaaaggagt ccggagtaaa 120
tcactattcc gtgccttttcg acggacattc agggccggtg aggattgcga ttgtccgaca 180
tggtagagaa gttaagaccg caacagggcc tgctataacg gaagagtgca cggacggtaa 240
agtaaattgg aatgcatttg taggatcaag ttaatcgata taaaattgta ctagacacta 300
aaagcgttgg gataaatggt atctagataa cttgtatgat gtttgcaata tcgggggcctg 360
ttatcgccag gcccggcctc ccagccactg ataagcgtea ctctcagtt ctccgcatga 420
ccgcatcttc cttcgtctct ctccaactct cctctctgtc gatgtcctct tcaccatctc 480

tcttgtttcc	atataccttag	ccttttctatt	gcattttttat	ttatccttttg	aatatggcca	540
agaaaattct	gtctgacatc	caccaccatg	agtctaactt	ggcttaccgc	cagtatgccc	600
agctgcctga	aaccctccac	ctcaactacc	agcctcctac	tgctactgca	acccccgcgc	660
cacacaccag	cccgatccca	gaggcaatca	accccgacga	ttactcgcag	gcttactgcg	720
attttatgac	tgagcatccc	accatttttc	acgcagtcga	tggcttctct	aagcaactcg	780
aaagcaaggg	atacaagtac	ctatccgagc	gggaattatg	gacgccgcag	ctcaaacgcg	840
gaggaaagta	ctatacgact	cgcaatggaa	gctcgttgat	tgcgttctct	gtcggccccg	900
agtataagag	tgggaatggc	ctcgctatca	tcgccggcca	cattgatgcc	ctcacggcga	960
agctcaagcc	cgtctcaaaa	cttcccaata	aagctggata	cattcagatg	ggagttgctc	1020
cttatgccgg	cggctctgggc	aagacatggc	gggaccgtga	tttgtctatc	ggcgggaagg	1080
ttctcgttcg	taacgctagc	accggcaagg	ttgaatccaa	gctagtcaag	ttgaactggc	1140
cgattgctcg	catcccaacg	ctagccgaac	actttggcgc	tccttcgcag	gggccattca	1200
acaaggaaac	acagatggta	cctatcattg	gagtcgacaa	ctctgatctt	ttccagtcta	1260
ccactccagc	ggcagacgag	ggcatcgaac	ccggcacctt	tgccctctacg	cagcccccaa	1320
aactcatcaa	agtgatctcc	aaggaacttg	gaatcacaaa	ctacagcagc	attctcagct	1380
gggagctaga	actttatgac	agccagcctg	cacgtatcgg	cggatttgac	aaggatttta	1440
tcttcgccgg	ccgcatacgat	gacaagctct	gctgctacgc	cgcacaggaa	gccctcatgg	1500
ctacctccga	ccacacctct	ccctcttcca	tcaagatggc	cggttacttt	gatgatgagg	1560
aaattggtag	cttgctccgt	cagggtgccc	gctccaactt	catgtctagc	gtcatcgaac	1620
gcattgcaca	atcctttgca	acatcatatg	gacccgatct	ccttgcccaa	accgttgcaa	1680
agagcttcct	tatctcttct	gatgtcatcc	acgctgtcaa	tcccaacttc	ttgaatgtct	1740
atctcgagaa	ccacgcgcct	cgtctcaatg	tcggcgtctc	cgtctccgca	gactcaaacg	1800
gccacatgac	taccgacagt	gtcagctacg	gcttcatcaa	gcgcgttgct	gaaaagtgcg	1860
gctctcagct	gcaggtcttt	caaatccgaa	atgactcccc	aagcggcgga	accattgggc	1920
ccatgaccag	ctcgcggatt	ggaatgaggg	ccattgatgt	cggatatcca	cagttgagca	1980
tgcatagcat	tcgcgccacc	acagggagtc	gcgatcctgg	gctgggtgtc	aagctgttta	2040

aggggttctt tgattacttt gaagaggtgg atcgtgagtt ttctgatttt taggttgtga	2100
ctcttgtttt ctgtcgaggg gtgctgtcgc gctgcttggc cgtgtctagt ttggtttgca	2160
tgattttggg gctaggggtg aagtgccttg gcattaagaa cctcatttag aatggtgact	2220
tctttgtata cggggttcgg agtccgtcta tagaggcatg tgtaaggata aaaatcgaat	2280
cctacataat tccaggctat gcacttgaac agacaacatc tagattctag gcacgtcaaa	2340
ccatacaata tattaagagg cttccgtcta tttgatgctc cacccggcac gaatctcaac	2400
agtaagcccc gtagtctact ccgtacttct tgccctgccga aggagaggat ggagatgagg	2460
gtgacgaatg cgttgttttc accagtgcc caatgacagt tgcattatcc tcaatttaat	2520
cagccccgtc tccttccagt tccaccccag cctttggagc agtccgggca atgctctctg	2580
cgacacttac tgtcatgatc cccctacata aacacacggc ttgcgagccc cagccccagc	2640
cccattcagg gccaaaagct ctagactgat ccgcatccca ctcacaactc ccatgttcca	2700
aatcattgat gtgcgttgtg attgtagtag aaatgcccat tccccaatg ctccagaaaa	2760
ctggcgggccg gggttcttgc ccaactgtaa gcgctaggct ccgagataat ctcttagact	2820
tggatttcga tctggatctg gggttgctgt gcgatgagag gagttgtgga atcatacggg	2880
aaagcagggg ccgcagagtc ggtaggcagg cgcagactat gccgacgttg cattccactg	2940
cggaccaggt tgcggcaccg acgttgatcat ctgcttgctg ttagtagggg tttttttggg	3000
ttgatggagg gacgtacagg ttgggtccga agagtcagcg attcttttta gggacatcaa	3060
acggcaaagt cttgttatgc agacgctaga attactcagg attagcagat gcacacaccg	3120
accatggaac agaaaacgta caaaccccc accgcaaaaa ttgcaataag agcaactctc	3180
tgcttccttg gcaaatcaag actatacaag gcaggtatag ggataactag gatagcaagg	3240
tccgtcgcaa tatgcattga agcattggag aaccacagag ccttcgaact gagacatgat	3300
cccgggattg ttgggtccca gaaacgtgct actggtatgc agttcaagaa cccgctaagc	3360
acagcccatg tgccgattga cga	3383

<210> 2
 <211> 1916
 <212> DNA

<213> Aspergillus nidulans

<220>

<221> CDS

<222> (72)..(1628)

<400> 2

```
tgctcctcttc accatctctc ttgtttccat atccttagcc tttctattgc atttttattt      60
atctttttgaa t atg gcc aag aaa att ctg tct gac atc cac cac cat gag      110
      Met Ala Lys Lys Ile Leu Ser Asp Ile His His His Glu
      1              5              10

tct aac ttg gct tac cgc cag tat gcc cag ctg cct gaa acc ctc cac      158
Ser Asn Leu Ala Tyr Arg Gln Tyr Ala Gln Leu Pro Glu Thr Leu His
      15              20              25

ctc aac tac cag cct cct act gct act gca acc ccc gcc gca cac acc      206
Leu Asn Tyr Gln Pro Pro Thr Ala Thr Ala Thr Pro Ala Ala His Thr
      30              35              40              45

agc ccg atc cca gag gca atc aac ccc gac gat tac tcg cag gct tac      254
Ser Pro Ile Pro Glu Ala Ile Asn Pro Asp Asp Tyr Ser Gln Ala Tyr
      50              55              60

tgc gat ttt atg act gag cat ccc acc att ttt cac gca gtc gat ggc      302
Cys Asp Phe Met Thr Glu His Pro Thr Ile Phe His Ala Val Asp Gly
      65              70              75

ttc tct aag caa ctc gaa agc aag gga tac aag tac cta tcc gag cgg      350
Phe Ser Lys Gln Leu Glu Ser Lys Gly Tyr Lys Tyr Leu Ser Glu Arg
      80              85              90

gaa tta tgg acg ccg cag ctc aaa cgc gga gga aag tac tat acg act      398
Glu Leu Trp Thr Pro Gln Leu Lys Arg Gly Gly Lys Tyr Tyr Thr Thr
      95              100              105

cgc aat gga agc tcg ttg att gcg ttc tct gtc ggc ccc gag tat aag      446
Arg Asn Gly Ser Ser Leu Ile Ala Phe Ser Val Gly Pro Glu Tyr Lys
      110              115              120              125

agt ggg aat ggc ctc gct atc atc gcc ggc cac att gat gcc ctc acg      494
Ser Gly Asn Gly Leu Ala Ile Ile Ala Gly His Ile Asp Ala Leu Thr
      130              135              140

gcg aag ctc aag ccc gtc tca aaa ctt ccc aat aaa gct gga tac att      542
Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Tyr Ile
      145              150              155

cag atg gga gtt gct cct tat gcc ggc ggt ctg ggc aag aca tgg tgg      590
```

Gln	Met	Gly	Val	Ala	Pro	Tyr	Ala	Gly	Gly	Leu	Gly	Lys	Thr	Trp	Trp	
		160					165					170				
gac	cgt	gat	ttg	tct	atc	ggc	ggg	aag	gtt	ctc	gtt	cgt	aac	gct	agc	638
Asp	Arg	Asp	Leu	Ser	Ile	Gly	Gly	Lys	Val	Leu	Val	Arg	Asn	Ala	Ser	
	175					180					185					
acc	ggc	aag	gtt	gaa	tcc	aag	cta	gtc	aag	ttg	aac	tgg	ccg	att	gct	686
Thr	Gly	Lys	Val	Glu	Ser	Lys	Leu	Val	Lys	Leu	Asn	Trp	Pro	Ile	Ala	
190					195					200					205	
cgc	atc	cca	acg	cta	gcc	gaa	cac	ttt	ggc	gct	cct	tcg	cag	ggg	cca	734
Arg	Ile	Pro	Thr	Leu	Ala	Glu	His	Phe	Gly	Ala	Pro	Ser	Gln	Gly	Pro	
				210					215					220		
ttc	aac	aag	gaa	aca	cag	atg	gta	cct	atc	att	gga	gtc	gac	aac	tct	782
Phe	Asn	Lys	Glu	Thr	Gln	Met	Val	Pro	Ile	Ile	Gly	Val	Asp	Asn	Ser	
			225					230					235			
gat	ctt	ttc	cag	tct	acc	act	cca	gcg	gca	gac	gag	ggc	atc	gaa	ccc	830
Asp	Leu	Phe	Gln	Ser	Thr	Thr	Pro	Ala	Ala	Asp	Glu	Gly	Ile	Glu	Pro	
		240					245					250				
ggc	acc	ttt	gcc	tct	acg	cag	ccc	cca	aaa	ctc	atc	aaa	gtg	atc	tcc	878
Gly	Thr	Phe	Ala	Ser	Thr	Gln	Pro	Pro	Lys	Leu	Ile	Lys	Val	Ile	Ser	
	255					260					265					
aag	gaa	ctt	gga	atc	aca	aac	tac	agc	agc	att	ctc	agc	tgg	gag	cta	926
Lys	Glu	Leu	Gly	Ile	Thr	Asn	Tyr	Ser	Ser	Ile	Leu	Ser	Trp	Glu	Leu	
270					275					280					285	
gaa	ctt	tat	gac	agc	cag	cct	gca	cgt	atc	ggc	ggt	att	gac	aag	gat	974
Glu	Leu	Tyr	Asp	Ser	Gln	Pro	Ala	Arg	Ile	Gly	Gly	Ile	Asp	Lys	Asp	
				290					295					300		
ttt	atc	ttc	gcc	ggc	cgc	atc	gat	gac	aag	ctc	tgc	tgc	tac	gcc	gca	1022
Phe	Ile	Phe	Ala	Gly	Arg	Ile	Asp	Asp	Lys	Leu	Cys	Cys	Tyr	Ala	Ala	
			305					310					315			
cag	gaa	gcc	ctc	atg	gct	acc	tcc	gac	cac	acc	tct	ccc	tct	tcc	atc	1070
Gln	Glu	Ala	Leu	Met	Ala	Thr	Ser	Asp	His	Thr	Ser	Pro	Ser	Ser	Ile	
		320					325					330				
aag	atg	gtc	ggt	tac	ttt	gat	gat	gag	gaa	att	ggt	agc	ttg	ctc	cgt	1118
Lys	Met	Val	Gly	Tyr	Phe	Asp	Asp	Glu	Glu	Ile	Gly	Ser	Leu	Leu	Arg	
	335					340					345					
cag	ggt	gcc	cgc	tcc	aac	ttc	atg	tct	agc	gtc	atc	gaa	cgc	att	gca	1166
Gln	Gly	Ala	Arg	Ser	Asn	Phe	Met	Ser	Ser	Val	Ile	Glu	Arg	Ile	Ala	
350					355					360					365	

caa tcc ttt gca aca tca tat gga ccc gat ctc ctt gcc caa acc gtt	1214
Gln Ser Phe Ala Thr Ser Tyr Gly Pro Asp Leu Leu Ala Gln Thr Val	
370 375 380	
gca aag agc ttc ctt atc tct tct gat gtc atc cac gct gtc aat ccc	1262
Ala Lys Ser Phe Leu Ile Ser Ser Asp Val Ile His Ala Val Asn Pro	
385 390 395	
aac ttc ttg aat gtc tat ctc gag aac cac gcg cct cgt ctc aat gtc	1310
Asn Phe Leu Asn Val Tyr Leu Glu Asn His Ala Pro Arg Leu Asn Val	
400 405 410	
ggc gtc tcc gtc tcc gca gac tca aac ggc cac atg act acc gac agt	1358
Gly Val Ser Val Ser Ala Asp Ser Asn Gly His Met Thr Thr Asp Ser	
415 420 425	
gtc agc tac ggc ttc atc aag cgc gtt gct gaa aag tgc ggc tct cag	1406
Val Ser Tyr Gly Phe Ile Lys Arg Val Ala Glu Lys Cys Gly Ser Gln	
430 435 440 445	
ctg cag gtc ttt caa atc cga aat gac tcc cga agc ggc gga acc att	1454
Leu Gln Val Phe Gln Ile Arg Asn Asp Ser Arg Ser Gly Gly Thr Ile	
450 455 460	
ggg ccc atg acc agc tcg cgg att gga atg agg gcc att gat gtc ggt	1502
Gly Pro Met Thr Ser Ser Arg Ile Gly Met Arg Ala Ile Asp Val Gly	
465 470 475	
atc cca cag ttg agc atg cat agc att cgc gcc acc aca ggg agt cgc	1550
Ile Pro Gln Leu Ser Met His Ser Ile Arg Ala Thr Thr Gly Ser Arg	
480 485 490	
gat cct ggg ctg ggt gtc aag ctg ttt aag ggg ttc ttt gat tac ttt	1598
Asp Pro Gly Leu Gly Val Lys Leu Phe Lys Gly Phe Phe Asp Tyr Phe	
495 500 505	
gaa gag gtg gat cgt gag ttt tct gat ttt taggttggtga ctcttggttt	1648
Glu Glu Val Asp Arg Glu Phe Ser Asp Phe	
510 515	
ctgtcgaggg gtgctgtcgc gctgcttggc cgtgtctagt ttggtttgca tgattttggt	1708
gctaggggttg aagtgcttgg gcattaagaa cctcatttag aatgggtgact tctttgtata	1768
cggggttcgg agtccgtcta tagaggcatg tgtaaggata aaaatcgaat cctacataat	1828
tccaggctat gcacttgaac agacaacatc tagattctag gcacgtcaaa ccatacaata	1888
tattaagagg cttccgtcta tttgatgc	1916

<210> 3
 <211> 519
 <212> PRT
 <213> Aspergillus nidulans

<400> 3

Met Ala Lys Lys Ile Leu Ser Asp Ile His His His Glu Ser Asn Leu
 1 5 10 15

Ala Tyr Arg Gln Tyr Ala Gln Leu Pro Glu Thr Leu His Leu Asn Tyr
 20 25 30

Gln Pro Pro Thr Ala Thr Ala Thr Pro Ala Ala His Thr Ser Pro Ile
 35 40 45

Pro Glu Ala Ile Asn Pro Asp Asp Tyr Ser Gln Ala Tyr Cys Asp Phe
 50 55 60

Met Thr Glu His Pro Thr Ile Phe His Ala Val Asp Gly Phe Ser Lys
 65 70 75 80

Gln Leu Glu Ser Lys Gly Tyr Lys Tyr Leu Ser Glu Arg Glu Leu Trp
 85 90 95

Thr Pro Gln Leu Lys Arg Gly Gly Lys Tyr Tyr Thr Thr Arg Asn Gly
 100 105 110

Ser Ser Leu Ile Ala Phe Ser Val Gly Pro Glu Tyr Lys Ser Gly Asn
 115 120 125

Gly Leu Ala Ile Ile Ala Gly His Ile Asp Ala Leu Thr Ala Lys Leu
 130 135 140

Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Tyr Ile Gln Met Gly
 145 150 155 160

Val Ala Pro Tyr Ala Gly Gly Leu Gly Lys Thr Trp Trp Asp Arg Asp
 165 170 175

Leu Ser Ile Gly Gly Lys Val Leu Val Arg Asn Ala Ser Thr Gly Lys
180 185 190

Val Glu Ser Lys Leu Val Lys Leu Asn Trp Pro Ile Ala Arg Ile Pro
195 200 205

Thr Leu Ala Glu His Phe Gly Ala Pro Ser Gln Gly Pro Phe Asn Lys
210 215 220

Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn Ser Asp Leu Phe
225 230 235 240

Gln Ser Thr Thr Pro Ala Ala Asp Glu Gly Ile Glu Pro Gly Thr Phe
245 250 255

Ala Ser Thr Gln Pro Pro Lys Leu Ile Lys Val Ile Ser Lys Glu Leu
260 265 270

Gly Ile Thr Asn Tyr Ser Ser Ile Leu Ser Trp Glu Leu Glu Leu Tyr
275 280 285

Asp Ser Gln Pro Ala Arg Ile Gly Gly Ile Asp Lys Asp Phe Ile Phe
290 295 300

Ala Gly Arg Ile Asp Asp Lys Leu Cys Cys Tyr Ala Ala Gln Glu Ala
305 310 315 320

Leu Met Ala Thr Ser Asp His Thr Ser Pro Ser Ser Ile Lys Met Val
325 330 335

Gly Tyr Phe Asp Asp Glu Glu Ile Gly Ser Leu Leu Arg Gln Gly Ala
340 345 350

Arg Ser Asn Phe Met Ser Ser Val Ile Glu Arg Ile Ala Gln Ser Phe
355 360 365

Ala Thr Ser Tyr Gly Pro Asp Leu Leu Ala Gln Thr Val Ala Lys Ser
370 375 380

Phe Leu Ile Ser Ser Asp Val Ile His Ala Val Asn Pro Asn Phe Leu
 385 390 395 400

Asn Val Tyr Leu Glu Asn His Ala Pro Arg Leu Asn Val Gly Val Ser
 405 410 415

Val Ser Ala Asp Ser Asn Gly His Met Thr Thr Asp Ser Val Ser Tyr
 420 425 430

Gly Phe Ile Lys Arg Val Ala Glu Lys Cys Gly Ser Gln Leu Gln Val
 435 440 445

Phe Gln Ile Arg Asn Asp Ser Arg Ser Gly Gly Thr Ile Gly Pro Met
 450 455 460

Thr Ser Ser Arg Ile Gly Met Arg Ala Ile Asp Val Gly Ile Pro Gln
 465 470 475 480

Leu Ser Met His Ser Ile Arg Ala Thr Thr Gly Ser Arg Asp Pro Gly
 485 490 495

Leu Gly Val Lys Leu Phe Lys Gly Phe Phe Asp Tyr Phe Glu Glu Val
 500 505 510

Asp Arg Glu Phe Ser Asp Phe
 515

<210> 4
 <211> 1679
 <212> DNA
 <213> *Aspergillus oryzae*

<220>
 <221> CDS
 <222> (73)..(1602)

<400> 4
 caggcttaaa ccgcattccg acaagatatc tagcctttaa actaagaaat tttccaactc 60
 ctagccttcg ac atg acc aaa agg agt gtc ctt gat ctc cgt gat tct gcc 111

Met Thr Lys Arg Ser Val Leu Asp Leu Arg Asp Ser Ala
1 5 10

atg gct tat cgc ctg tcg gcc cag ctt cct gag ccc tcc cca gcc acc	159
Met Ala Tyr Arg Leu Ser Ala Gln Leu Pro Glu Pro Ser Pro Ala Thr	
15 20 25	
att gca acc cca gtg gcg agg agt ggc ccc ttc gcc ccg gaa gat tac	207
Ile Ala Thr Pro Val Ala Arg Ser Gly Pro Phe Ala Pro Glu Asp Tyr	
30 35 40 45	
acg aaa cca tac tgc gaa ttc atg aca gca aac ccc aca atc ttt cac	255
Thr Lys Pro Tyr Cys Glu Phe Met Thr Ala Asn Pro Thr Ile Phe His	
50 55 60	
gcc gtt gat ggt ttc acc agg cag ctc gaa agc cag gga tac aag cgc	303
Ala Val Asp Gly Phe Thr Arg Gln Leu Glu Ser Gln Gly Tyr Lys Arg	
65 70 75	
ctt ccc gag cgc gag acg tgg aac tcc aag tta gag aag ggt ggg aag	351
Leu Pro Glu Arg Glu Thr Trp Asn Ser Lys Leu Glu Lys Gly Gly Lys	
80 85 90	
tac tac gtc act cgg aat ggt agt gct ttc atc tca ttc tca att gga	399
Tyr Tyr Val Thr Arg Asn Gly Ser Ala Phe Ile Ser Phe Ser Ile Gly	
95 100 105	
aga gat tat aaa agt ggc aat gga atg gcc att gtt gca ggt cat atc	447
Arg Asp Tyr Lys Ser Gly Asn Gly Met Ala Ile Val Ala Gly His Ile	
110 115 120 125	
gat gca ctc acc gcc aaa ttg aag ccc gtg tcc aag ctg ccc aac aag	495
Asp Ala Leu Thr Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys	
130 135 140	
gct ggc ttt tcc cag ctc gga gtt gcg ccc tac gca ggc gct ctg agt	543
Ala Gly Phe Ser Gln Leu Gly Val Ala Pro Tyr Ala Gly Ala Leu Ser	
145 150 155	
gac aca tgg tgg gac cgc gat ctc tca ata ggt ggc cgt gtt ctg gtc	591
Asp Thr Trp Trp Asp Arg Asp Leu Ser Ile Gly Gly Arg Val Leu Val	
160 165 170	
caa gac tcc aac acc ggg aaa gtc gag tcc aaa tta gtc aaa ttg gac	639
Gln Asp Ser Asn Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asp	
175 180 185	
tgg ccc att gct cgg atc cca acc ctg gca cct cat ttc ggg gct ccc	687
Trp Pro Ile Ala Arg Ile Pro Thr Leu Ala Pro His Phe Gly Ala Pro	
190 195 200 205	

tcg	caa	ggc	ccc	ttc	aac	aaa	gag	act	cag	atg	gtg	cct	ata	att	ggc	735
Ser	Gln	Gly	Pro	Phe	Asn	Lys	Glu	Thr	Gln	Met	Val	Pro	Ile	Ile	Gly	
				210					215					220		
gtt	gat	aac	tcc	gat	ctt	ttc	cag	cag	caa	gcc	cca	tcc	aag	ata	gat	783
Val	Asp	Asn	Ser	Asp	Leu	Phe	Gln	Gln	Gln	Ala	Pro	Ser	Lys	Ile	Asp	
			225					230					235			
caa	gac	aac	ggg	atc	aaa	cct	ggt	aca	ttt	gca	gcc	acg	caa	ccg	gaa	831
Gln	Asp	Asn	Gly	Ile	Lys	Pro	Gly	Thr	Phe	Ala	Ala	Thr	Gln	Pro	Glu	
		240					245					250				
aag	ctt	gtc	aaa	gtc	ata	tcc	aag	gag	ctt	ggt	atc	aca	gac	tac	agc	879
Lys	Leu	Val	Lys	Val	Ile	Ser	Lys	Glu	Leu	Gly	Ile	Thr	Asp	Tyr	Ser	
	255					260					265					
tcg	att	ata	agc	tgg	gag	ctg	gag	ctg	tat	gac	agt	caa	cca	gca	caa	927
Ser	Ile	Ile	Ser	Trp	Glu	Leu	Glu	Leu	Tyr	Asp	Ser	Gln	Pro	Ala	Gln	
270					275					280					285	
gtt	ggt	ggc	ctg	gac	aag	gac	ctg	att	ttt	gct	ggt	cgc	att	gac	gat	975
Val	Gly	Gly	Leu	Asp	Lys	Asp	Leu	Ile	Phe	Ala	Gly	Arg	Ile	Asp	Asp	
			290						295					300		
aag	ctc	tgc	tgc	tat	gcc	gct	cag	gaa	gct	ctg	ctt	gcc	tca	tcc	gac	1023
Lys	Leu	Cys	Cys	Tyr	Ala	Ala	Gln	Glu	Ala	Leu	Leu	Ala	Ser	Ser	Asp	
			305					310					315			
agt	act	tca	act	agc	tct	atc	aag	atg	gtc	ggt	atg	ttt	gat	gac	gag	1071
Ser	Thr	Ser	Thr	Ser	Ser	Ile	Lys	Met	Val	Gly	Met	Phe	Asp	Asp	Glu	
		320					325					330				
gaa	att	gga	agc	ctg	ctt	cgc	cag	gga	gct	cga	tcc	aac	ttc	atg	agc	1119
Glu	Ile	Gly	Ser	Leu	Leu	Arg	Gln	Gly	Ala	Arg	Ser	Asn	Phe	Met	Ser	
	335					340					345					
agt	gtc	ata	gag	cgt	att	acg	gaa	gcc	ttc	tca	ccc	aat	tac	ggt	cct	1167
Ser	Val	Ile	Glu	Arg	Ile	Thr	Glu	Ala	Phe	Ser	Pro	Asn	Tyr	Gly	Pro	
350					355					360					365	
aac	gtg	ctg	tct	caa	act	gtg	gcg	aac	agc	ttc	ttc	gtg	tct	tcg	gac	1215
Asn	Val	Leu	Ser	Gln	Thr	Val	Ala	Asn	Ser	Phe	Phe	Val	Ser	Ser	Asp	
				370					375					380		
gtc	atc	cat	gcg	gtc	aat	ccg	aac	ttc	ctt	ggt	gtc	tat	ctt	gag	aac	1263
Val	Ile	His	Ala	Val	Asn	Pro	Asn	Phe	Leu	Gly	Val	Tyr	Leu	Glu	Asn	
			385					390					395			
cat	gct	ccc	cgt	ctg	aac	gtc	ggt	gtg	gcc	gtc	tcg	gct	gac	tct	aac	1311
His	Ala	Pro	Arg	Leu	Asn	Val	Gly	Val	Ala	Val	Ser	Ala	Asp	Ser	Asn	
		400					405					410				

ggc cat atg aca aca gac agt gtg agc tac gga ttc atc aag cgt gtc 1359
 Gly His Met Thr Thr Asp Ser Val Ser Tyr Gly Phe Ile Lys Arg Val
 415 420 425

gct gat cga tgt ggc tcg acc ttg cag gtc ttc cag att cgt aat gac 1407
 Ala Asp Arg Cys Gly Ser Thr Leu Gln Val Phe Gln Ile Arg Asn Asp
 430 435 440 445

tcc cgt agt ggc ggg act att gga ccc atg acc agt tct cgc att ggc 1455
 Ser Arg Ser Gly Gly Thr Ile Gly Pro Met Thr Ser Ser Arg Ile Gly
 450 455 460

atg agg gcc att gac gtg ggg atc ccg cag ttg agt atg cac agt atc 1503
 Met Arg Ala Ile Asp Val Gly Ile Pro Gln Leu Ser Met His Ser Ile
 465 470 475

cgt gcg act acc ggt agt ttg gat ccg gga ttg ggt gtg aag ctg ttc 1551
 Arg Ala Thr Thr Gly Ser Leu Asp Pro Gly Leu Gly Val Lys Leu Phe
 480 485 490

aag ggc ttt ttc gac tat ttc gag gag gtg gac aag gaa ttt gca gat 1599
 Lys Gly Phe Phe Asp Tyr Phe Glu Glu Val Asp Lys Glu Phe Ala Asp
 495 500 505

ttc tgatgcgctc ctctggaata ctaggaaatg tttccatcga taagtatgca 1652
 Phe
 510

ctatctggga ttccgatggt ggatctg 1679

<210> 5
 <211> 510
 <212> PRT
 <213> Aspergillus oryzae

<400> 5

Met Thr Lys Arg Ser Val Leu Asp Leu Arg Asp Ser Ala Met Ala Tyr
 1 5 10 15

Arg Leu Ser Ala Gln Leu Pro Glu Pro Ser Pro Ala Thr Ile Ala Thr
 20 25 30

Pro Val Ala Arg Ser Gly Pro Phe Ala Pro Glu Asp Tyr Thr Lys Pro
 35 40 45

Tyr Cys Glu Phe Met Thr Ala Asn Pro Thr Ile Phe His Ala Val Asp
50 55 60

Gly Phe Thr Arg Gln Leu Glu Ser Gln Gly Tyr Lys Arg Leu Pro Glu
65 70 75 80

Arg Glu Thr Trp Asn Ser Lys Leu Glu Lys Gly Gly Lys Tyr Tyr Val
85 90 95

Thr Arg Asn Gly Ser Ala Phe Ile Ser Phe Ser Ile Gly Arg Asp Tyr
100 105 110

Lys Ser Gly Asn Gly Met Ala Ile Val Ala Gly His Ile Asp Ala Leu
115 120 125

Thr Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Phe
130 135 140

Ser Gln Leu Gly Val Ala Pro Tyr Ala Gly Ala Leu Ser Asp Thr Trp
145 150 155 160

Trp Asp Arg Asp Leu Ser Ile Gly Gly Arg Val Leu Val Gln Asp Ser
165 170 175

Asn Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asp Trp Pro Ile
180 185 190

Ala Arg Ile Pro Thr Leu Ala Pro His Phe Gly Ala Pro Ser Gln Gly
195 200 205

Pro Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn
210 215 220

Ser Asp Leu Phe Gln Gln Gln Ala Pro Ser Lys Ile Asp Gln Asp Asn
225 230 235 240

Gly Ile Lys Pro Gly Thr Phe Ala Ala Thr Gln Pro Glu Lys Leu Val
245 250 255

Lys Val Ile Ser Lys Glu Leu Gly Ile Thr Asp Tyr Ser Ser Ile Ile
 260 265 270

Ser Trp Glu Leu Glu Leu Tyr Asp Ser Gln Pro Ala Gln Val Gly Gly
 275 280 285

Leu Asp Lys Asp Leu Ile Phe Ala Gly Arg Ile Asp Asp Lys Leu Cys
 290 295 300

Cys Tyr Ala Ala Gln Glu Ala Leu Leu Ala Ser Ser Asp Ser Thr Ser
 305 310 315 320

Thr Ser Ser Ile Lys Met Val Gly Met Phe Asp Asp Glu Glu Ile Gly
 325 330 335

Ser Leu Leu Arg Gln Gly Ala Arg Ser Asn Phe Met Ser Ser Val Ile
 340 345 350

Glu Arg Ile Thr Glu Ala Phe Ser Pro Asn Tyr Gly Pro Asn Val Leu
 355 360 365

Ser Gln Thr Val Ala Asn Ser Phe Phe Val Ser Ser Asp Val Ile His
 370 375 380

Ala Val Asn Pro Asn Phe Leu Gly Val Tyr Leu Glu Asn His Ala Pro
 385 390 395 400

Arg Leu Asn Val Gly Val Ala Val Ser Ala Asp Ser Asn Gly His Met
 405 410 415

Thr Thr Asp Ser Val Ser Tyr Gly Phe Ile Lys Arg Val Ala Asp Arg
 420 425 430

Cys Gly Ser Thr Leu Gln Val Phe Gln Ile Arg Asn Asp Ser Arg Ser
 435 440 445

Gly Gly Thr Ile Gly Pro Met Thr Ser Ser Arg Ile Gly Met Arg Ala
 450 455 460

Ile Asp Val Gly Ile Pro Gln Leu Ser Met His Ser Ile Arg Ala Thr
 465 470 475 480

Thr Gly Ser Leu Asp Pro Gly Leu Gly Val Lys Leu Phe Lys Gly Phe
 485 490 495

Phe Asp Tyr Phe Glu Glu Val Asp Lys Glu Phe Ala Asp Phe
 500 505 510

<210> 6
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 6
 ctcaaacggc cacatgacta c

21

<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 7
 gtctgttcaa gtgcatagcc tg

22

<210> 8
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 8
 caccacatg agtctaactt gg

22

<210> 9

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 9
gtctgttcaa gtgcatagcc tg

22

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 10
cgtggtacca tggcttagag t

21

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 11
aatcgacagta agcctgacgag

20

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 12
cgtggtacca tggcttagag t

21

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 13

catgggcca atggttccgc

20

<210> 14

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 14

ccagattcgt aatgactccc g

21

<210> 15

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 15

ctactactac taggccacgc gtcgactagt ac

32